FIG. 1

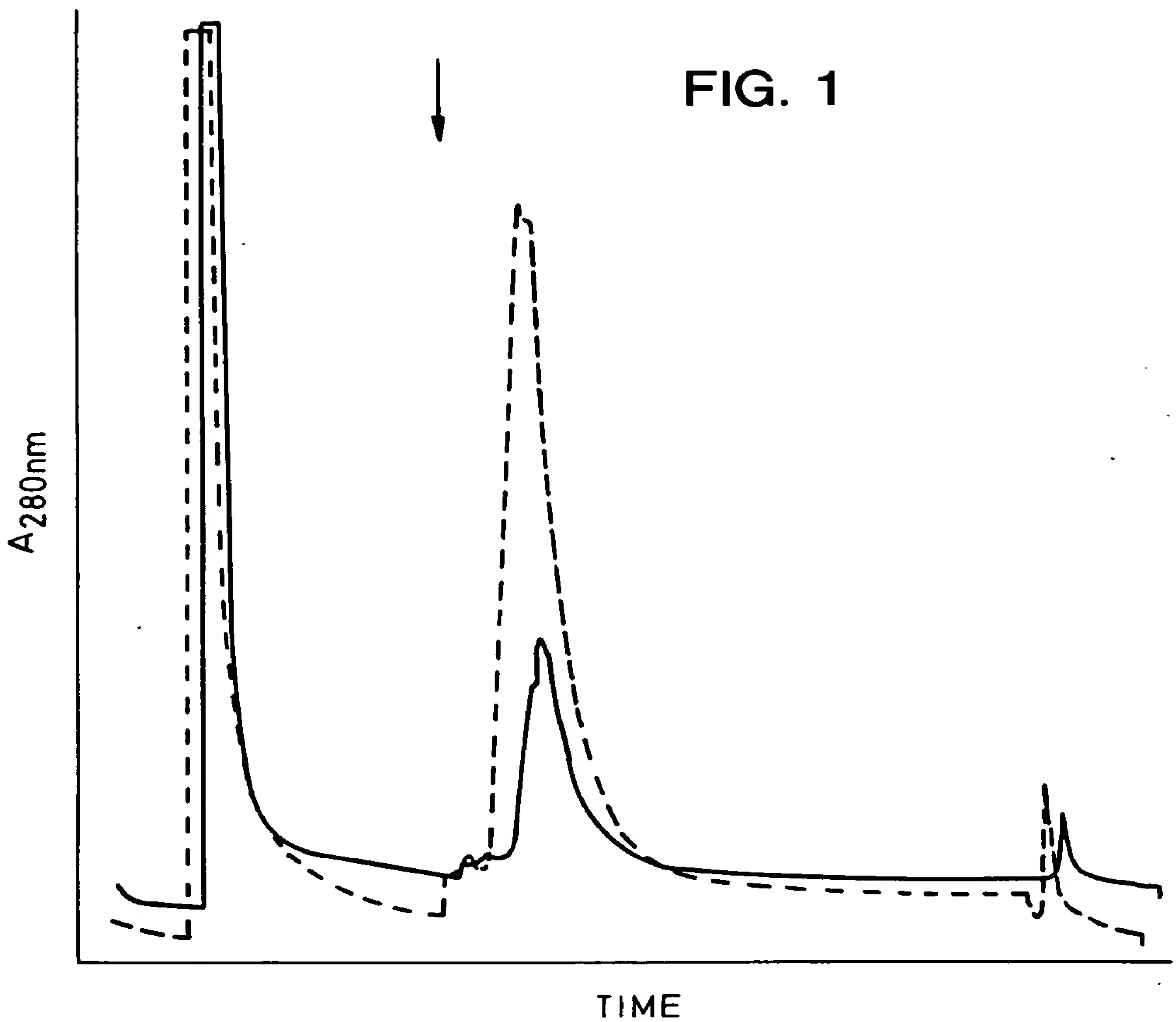


FIG. 2A

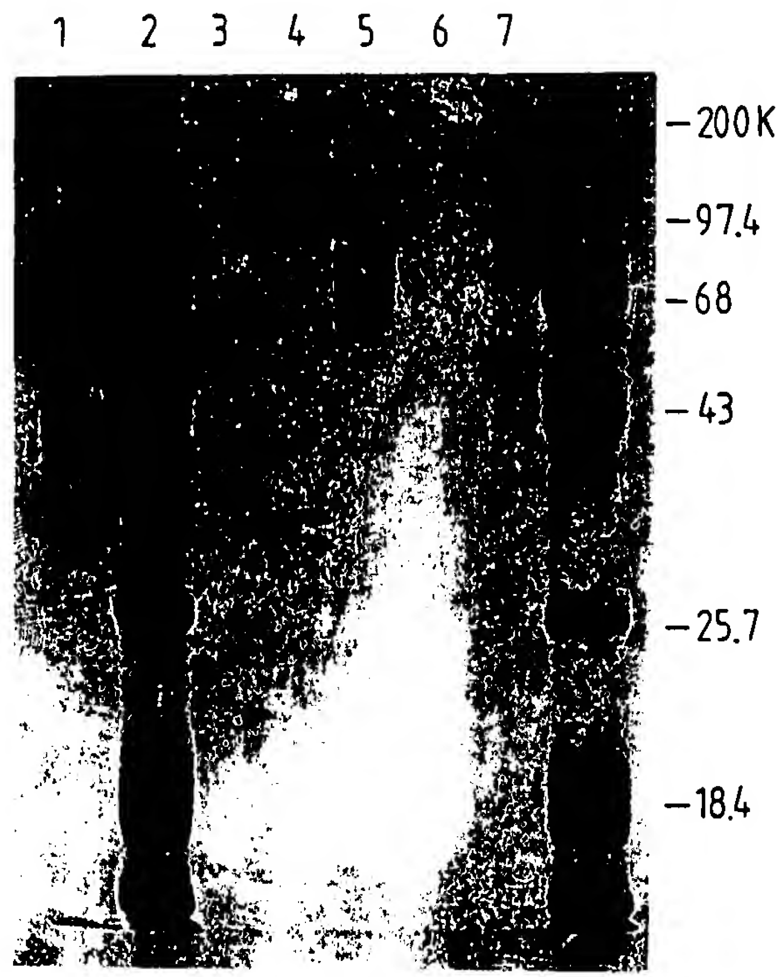


FIG. 2B

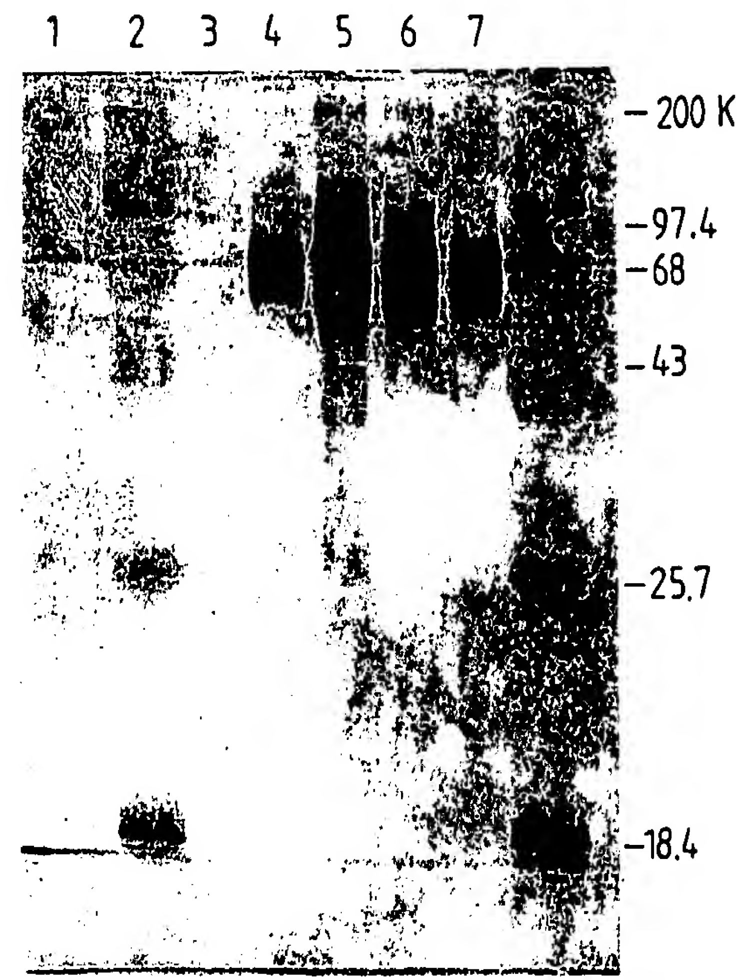
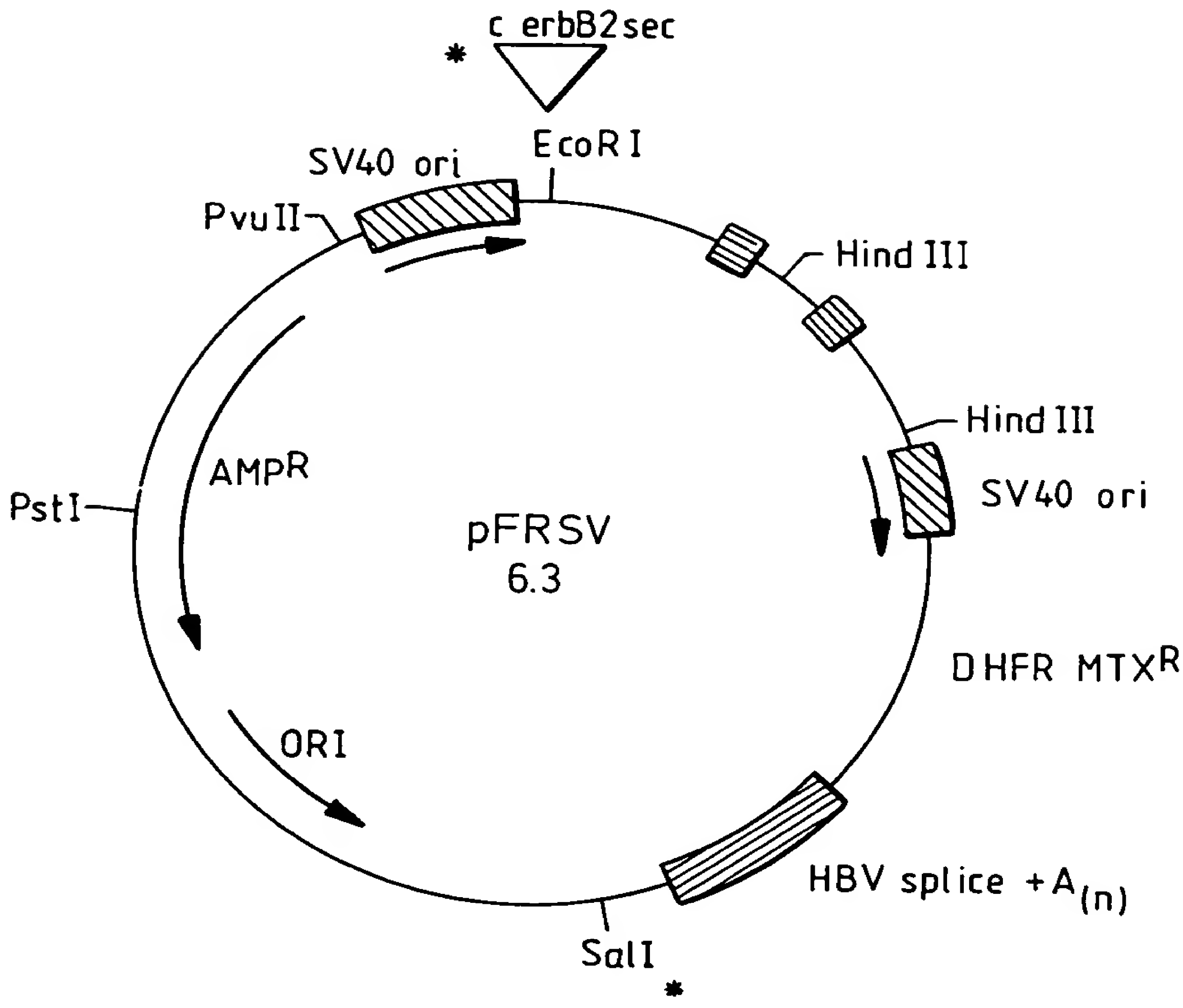
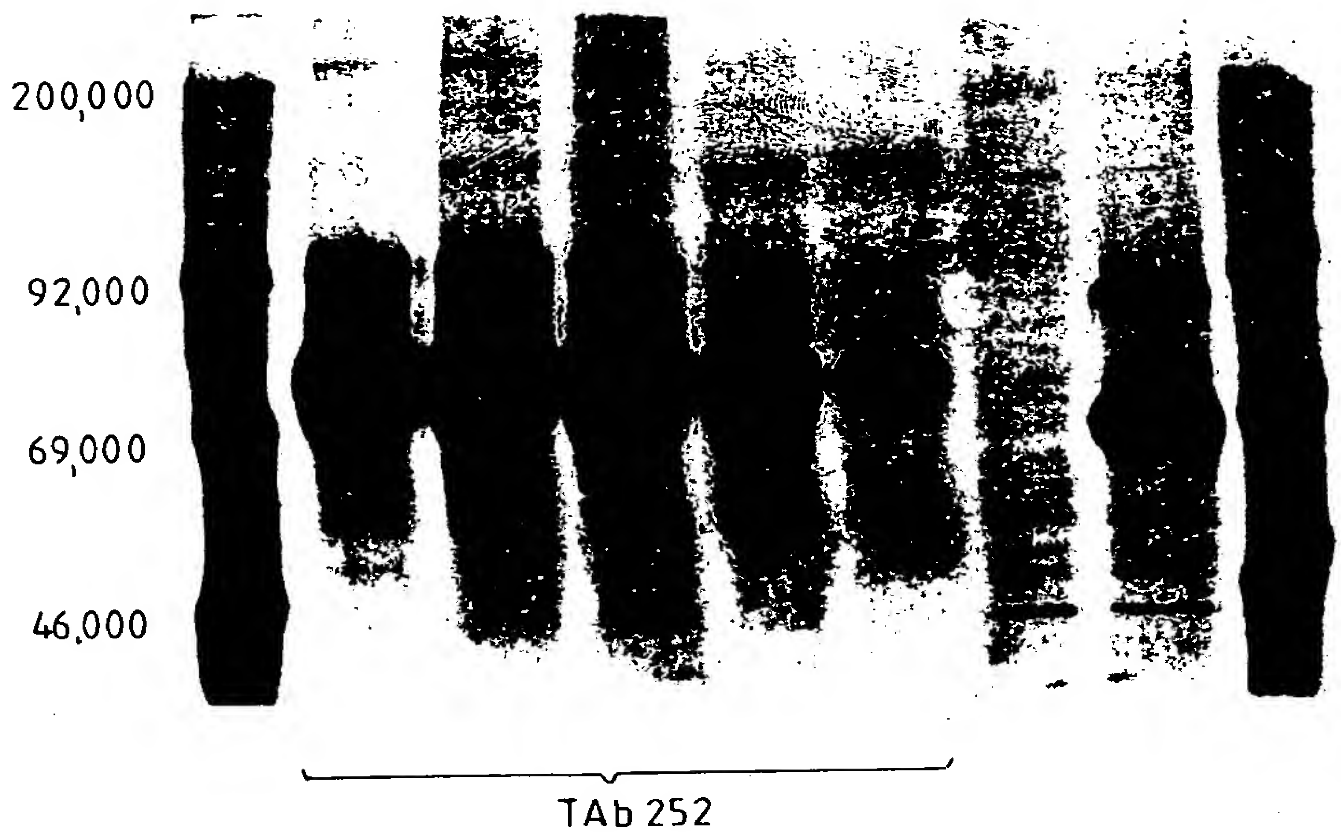


FIG. 3



c erbB2sec
EcoRI
SV40 ori
PvuII
HindIII
HindIII
SV40 ori
PstI
AMP^R
pFRSV
6.3
DHFR MTX^R
ORI
HBV splice +$A_{(n)}$
SalI

FIG. 4



NIH3T3-c-erbB-2 lysate + S35 labeled c1.4-3 supernatant

FIG. 5

Radioimmunoprecipitation of gp75 from SKBR3 Supernatant

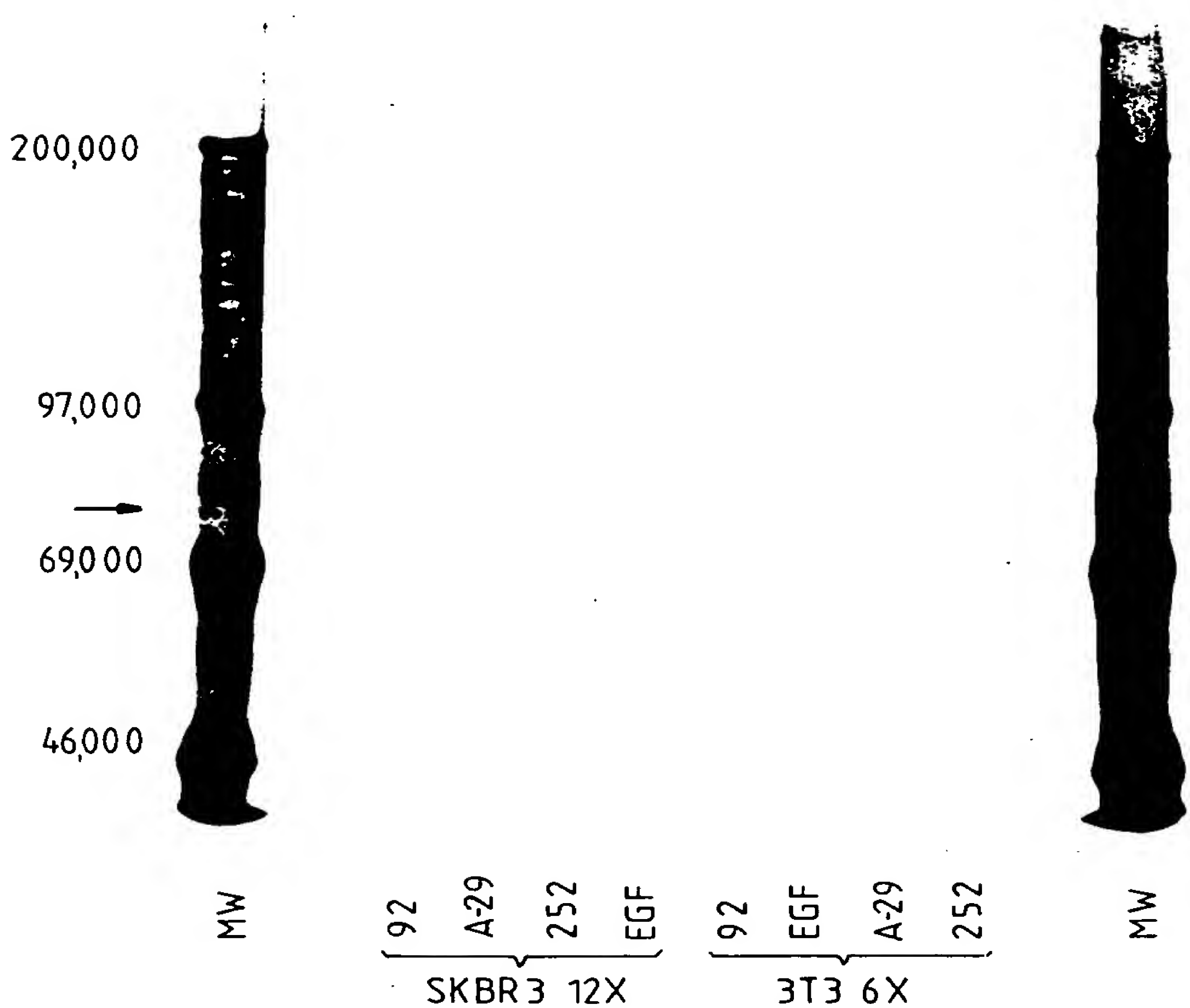


FIG. 6

Radioimmunoprecipitation of Supernatants From Various Cell Lines

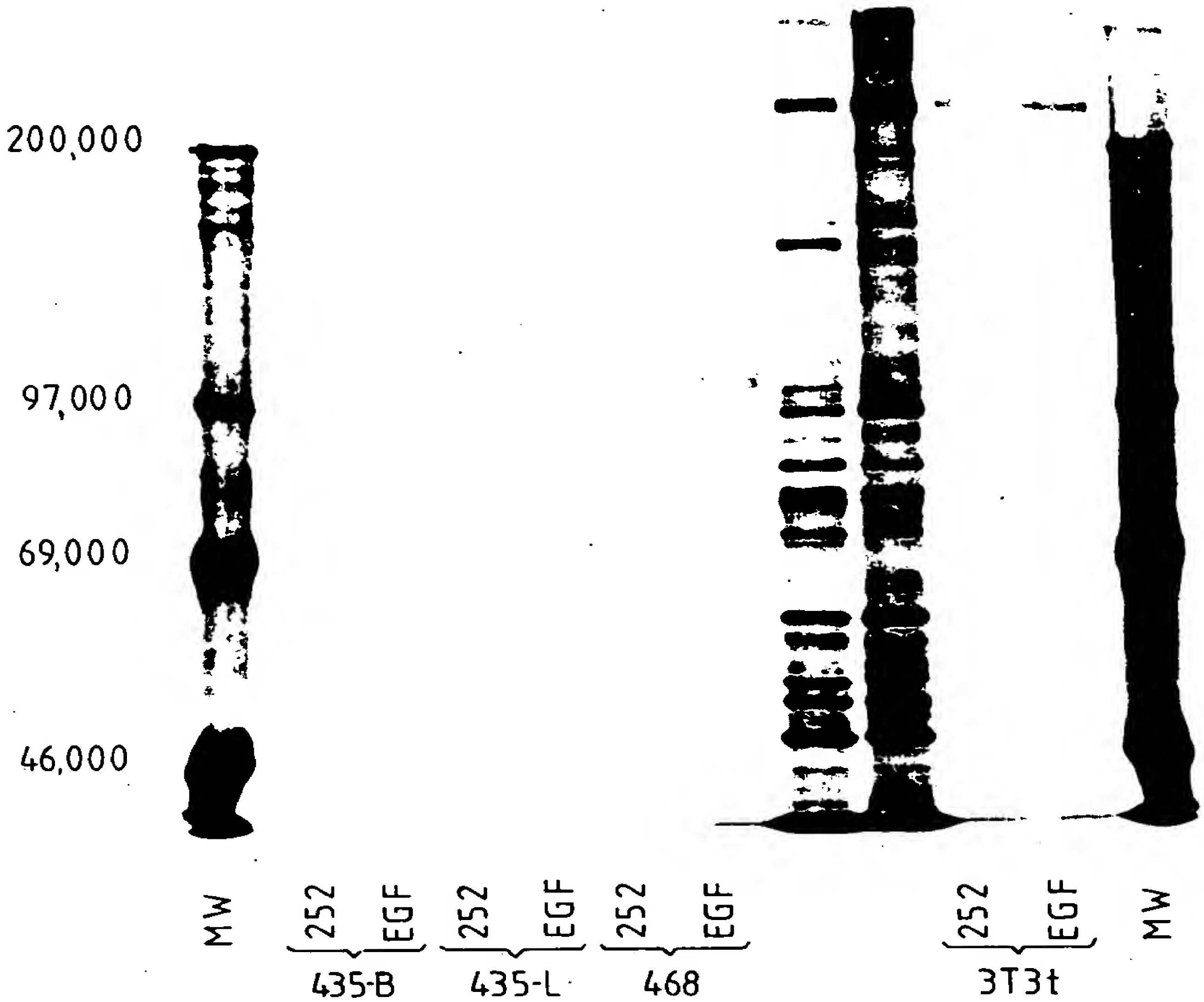


FIG. 7

Comparison of Standards in Sandwich IRMA

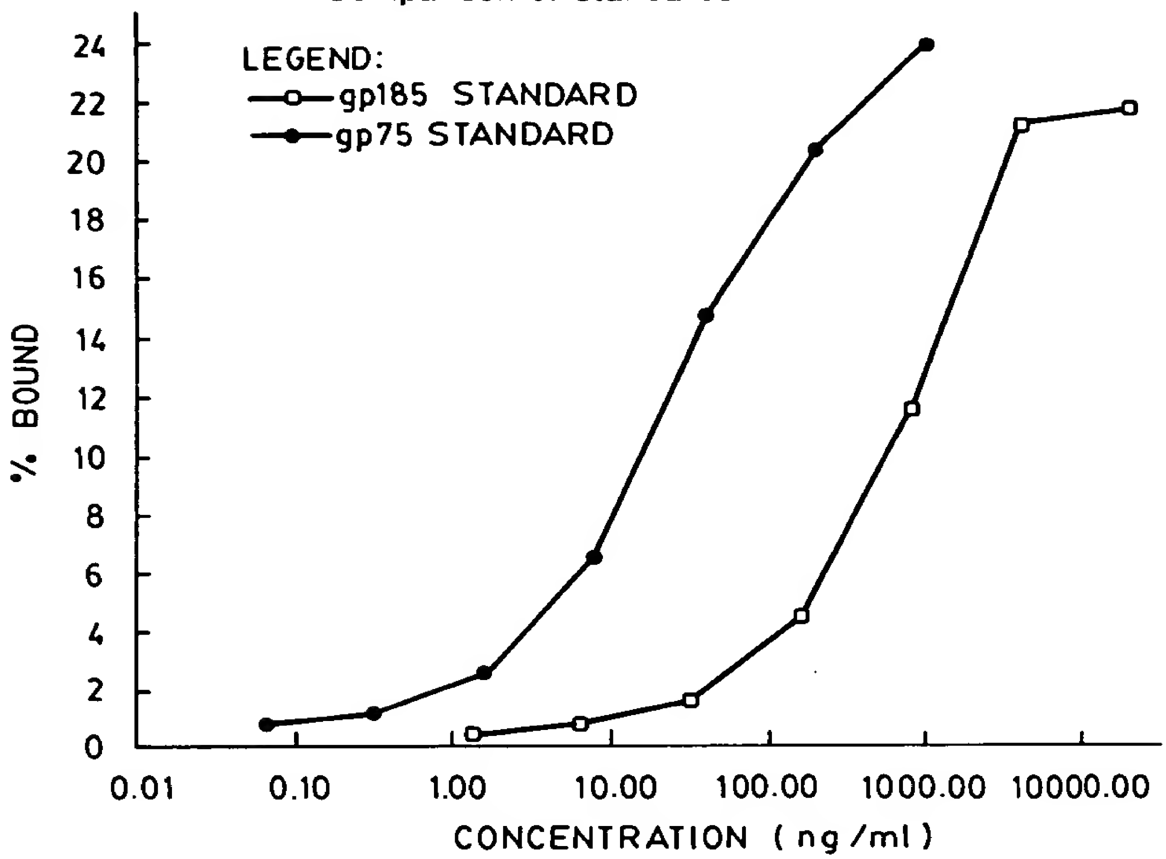


FIG. 8

Analysis of Nude Mouse Sera In c-erbB-2 IRMA

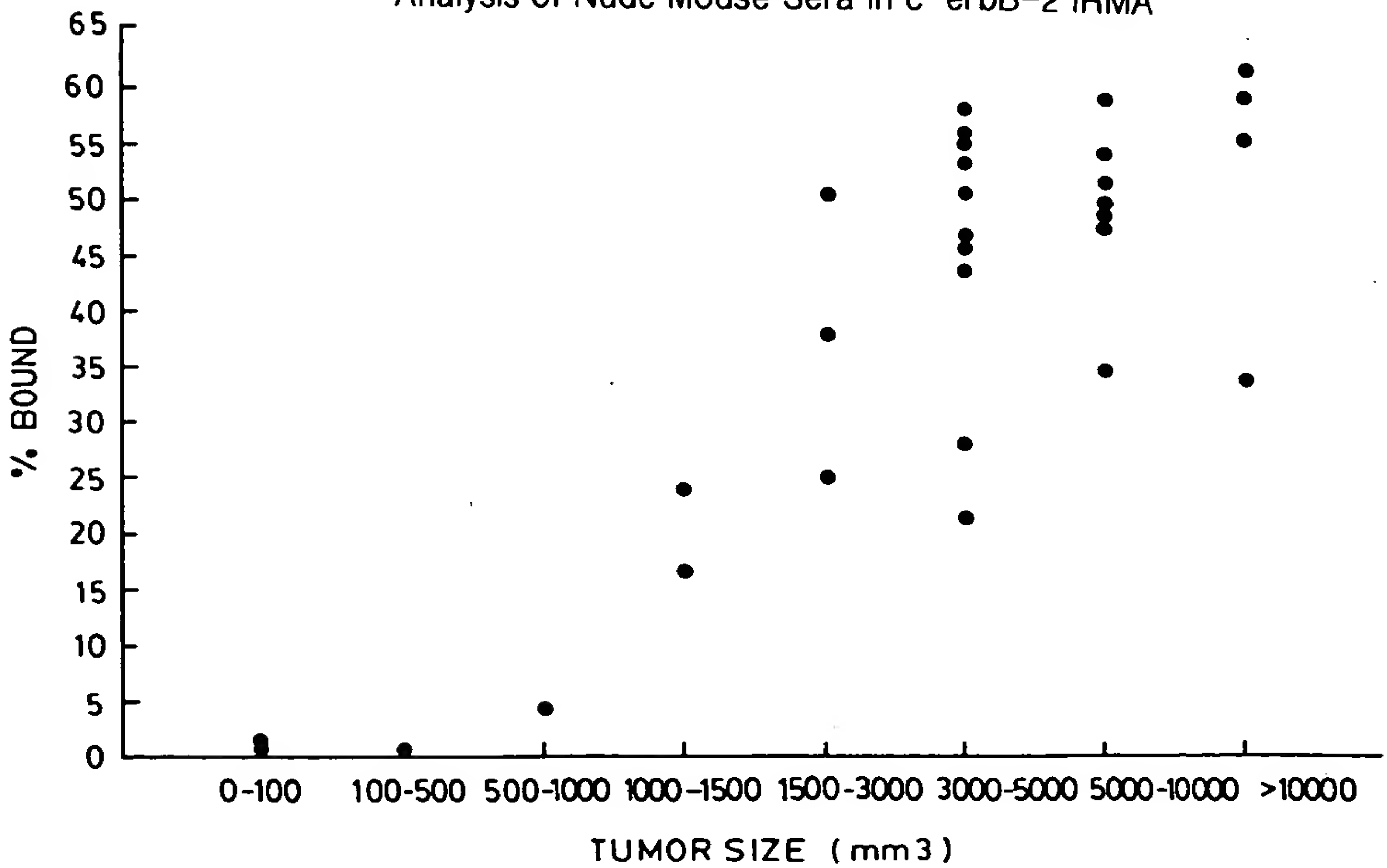


FIG. 9

Analysis of Nude Mouse Sera in the c-erbB-2 IRMA
Treated vs. Untreated

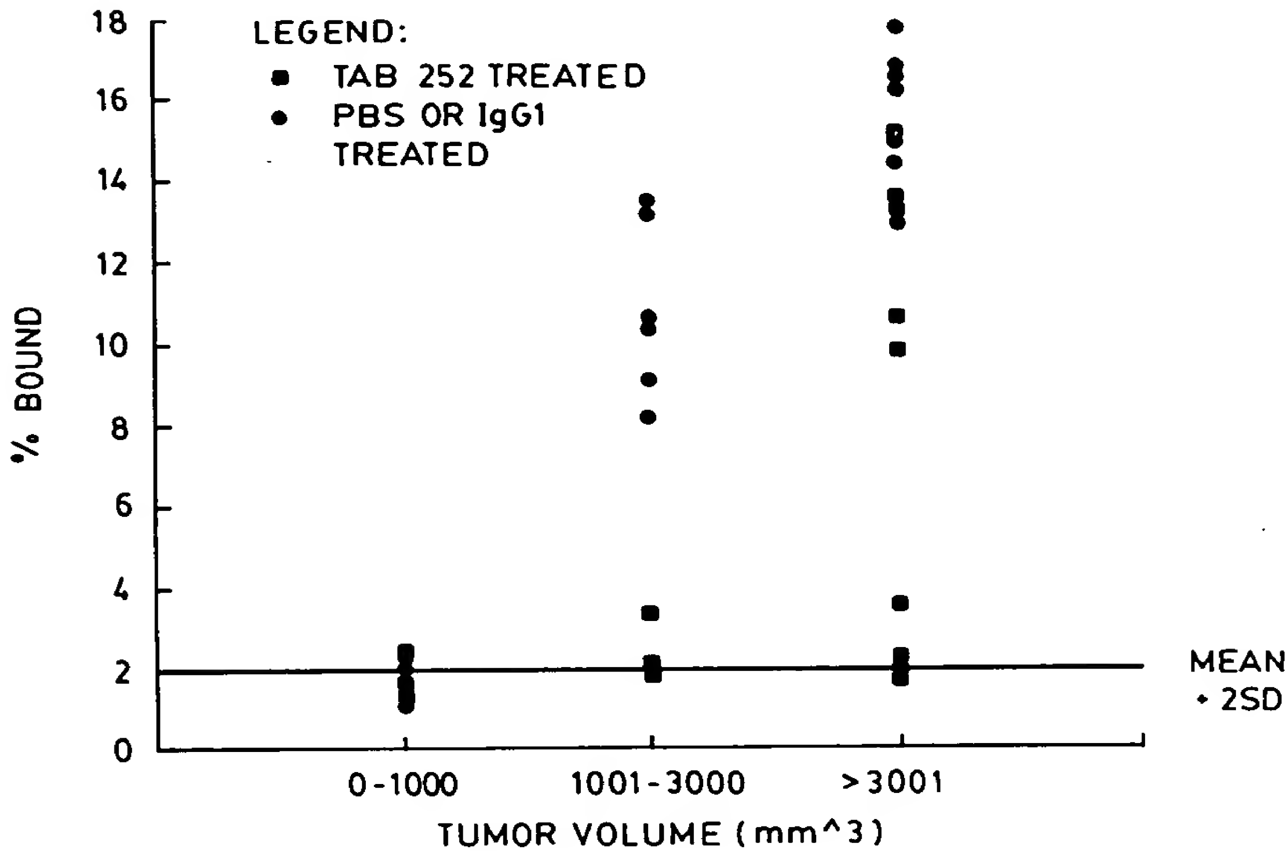


FIG. 10

Analysis of Normal Human Sera in the c-erbB-2 IRMA

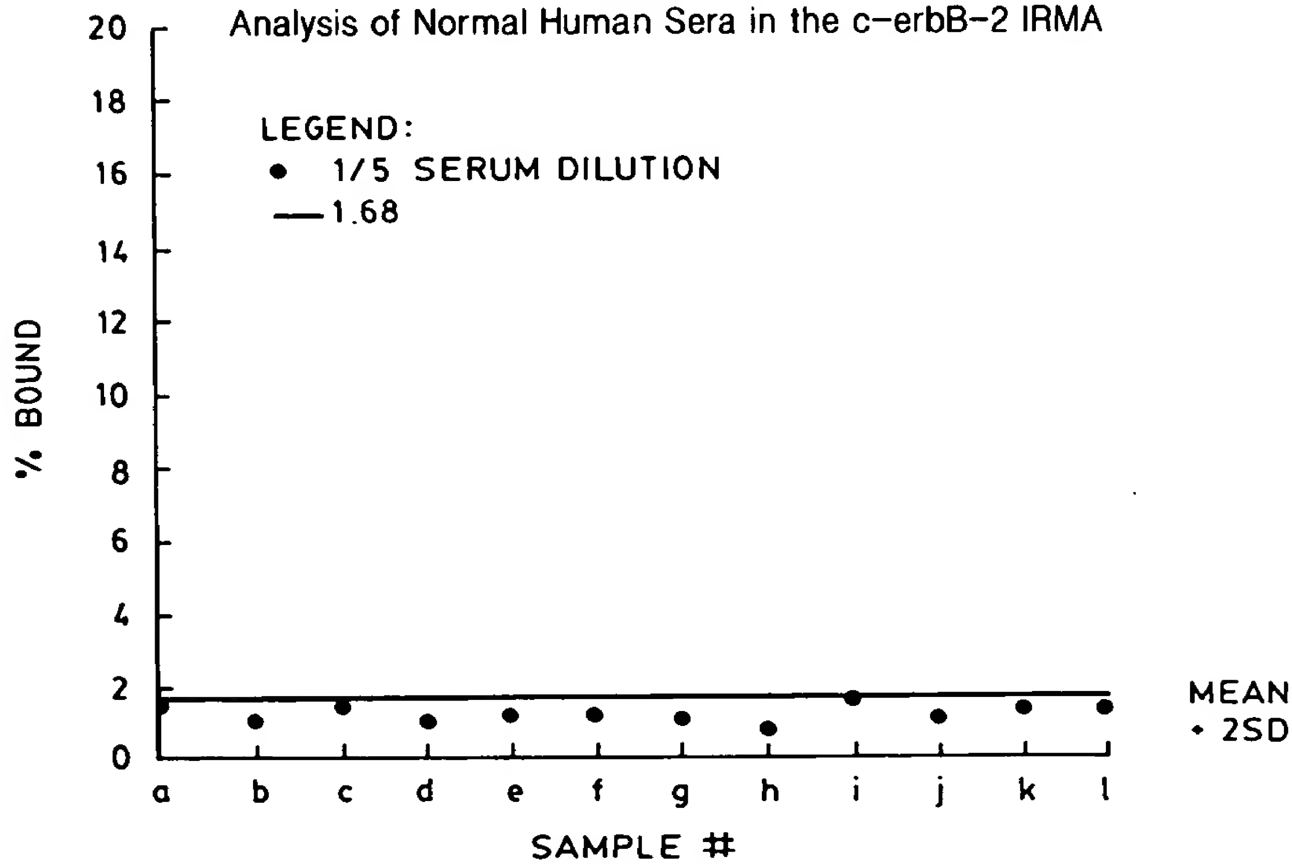


FIG. 11

Analysis of 20 Sera from Human Breast Cancer Patients
Serial Samples Assayed in the Sandwich IRMA

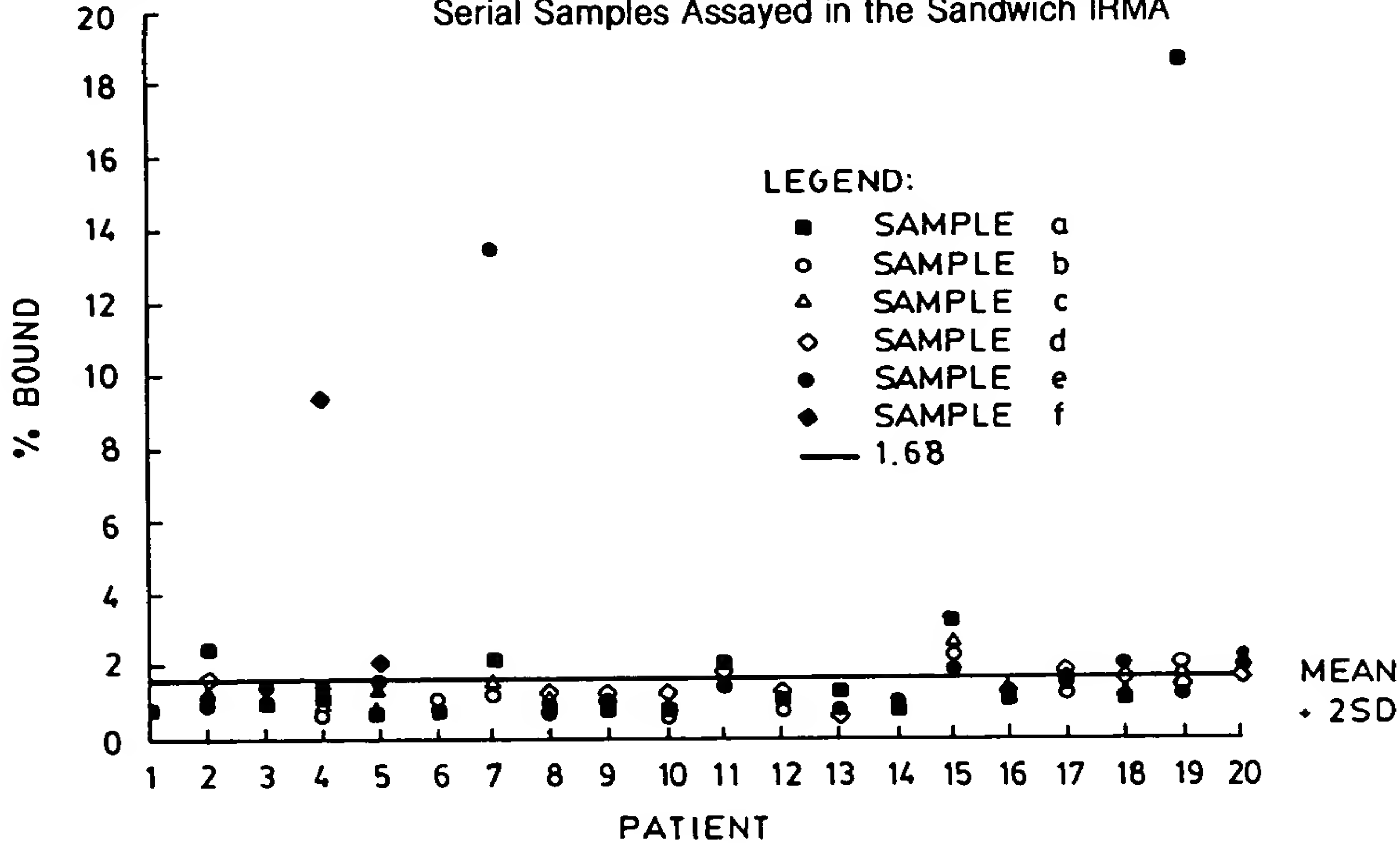


FIG. 12

Sandwich IRMA: Human Breast Sera and Control Sera

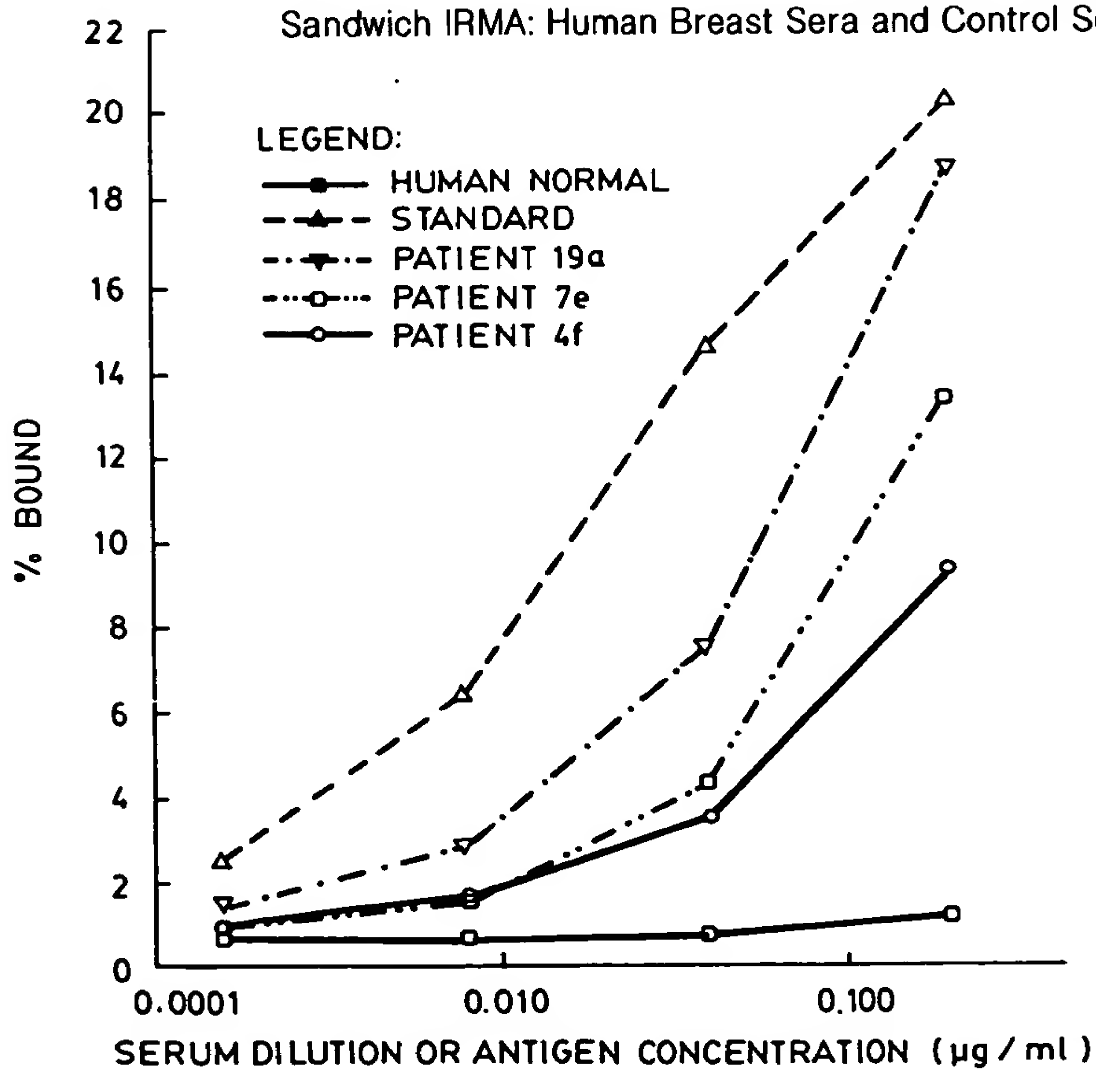


FIG. 13

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate

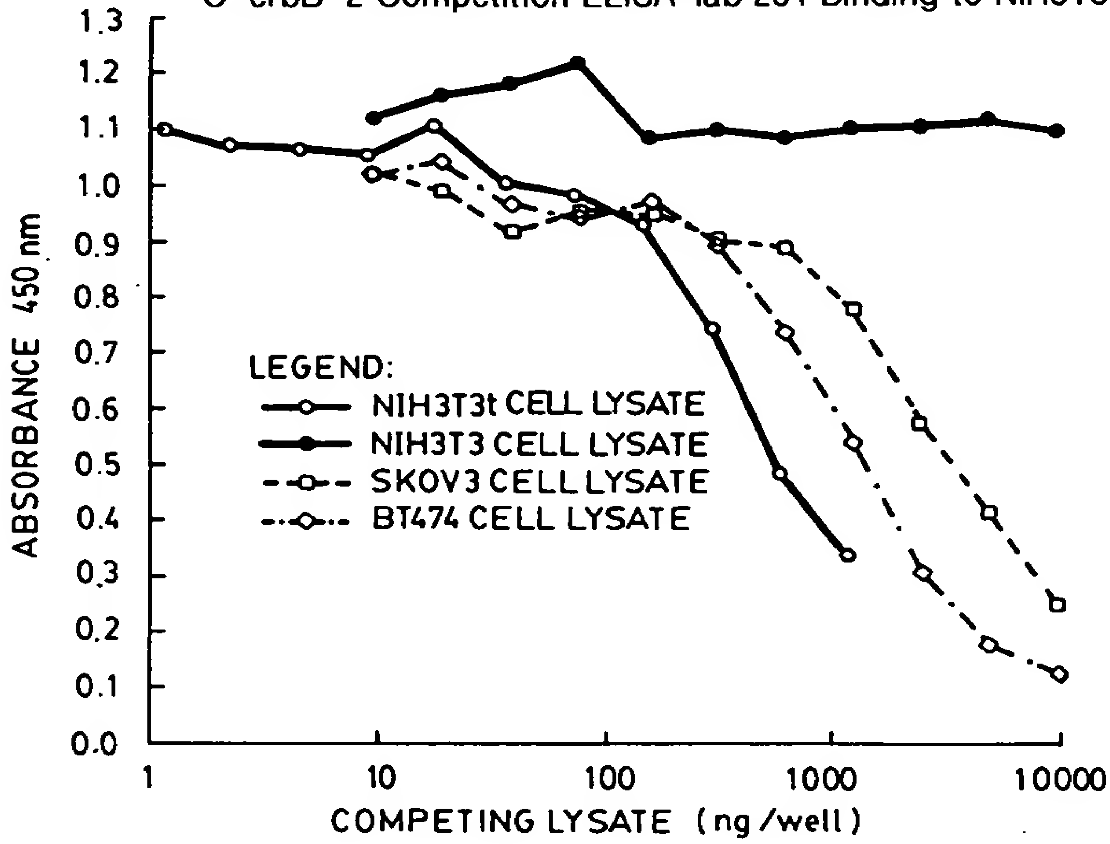


FIG. 14

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate

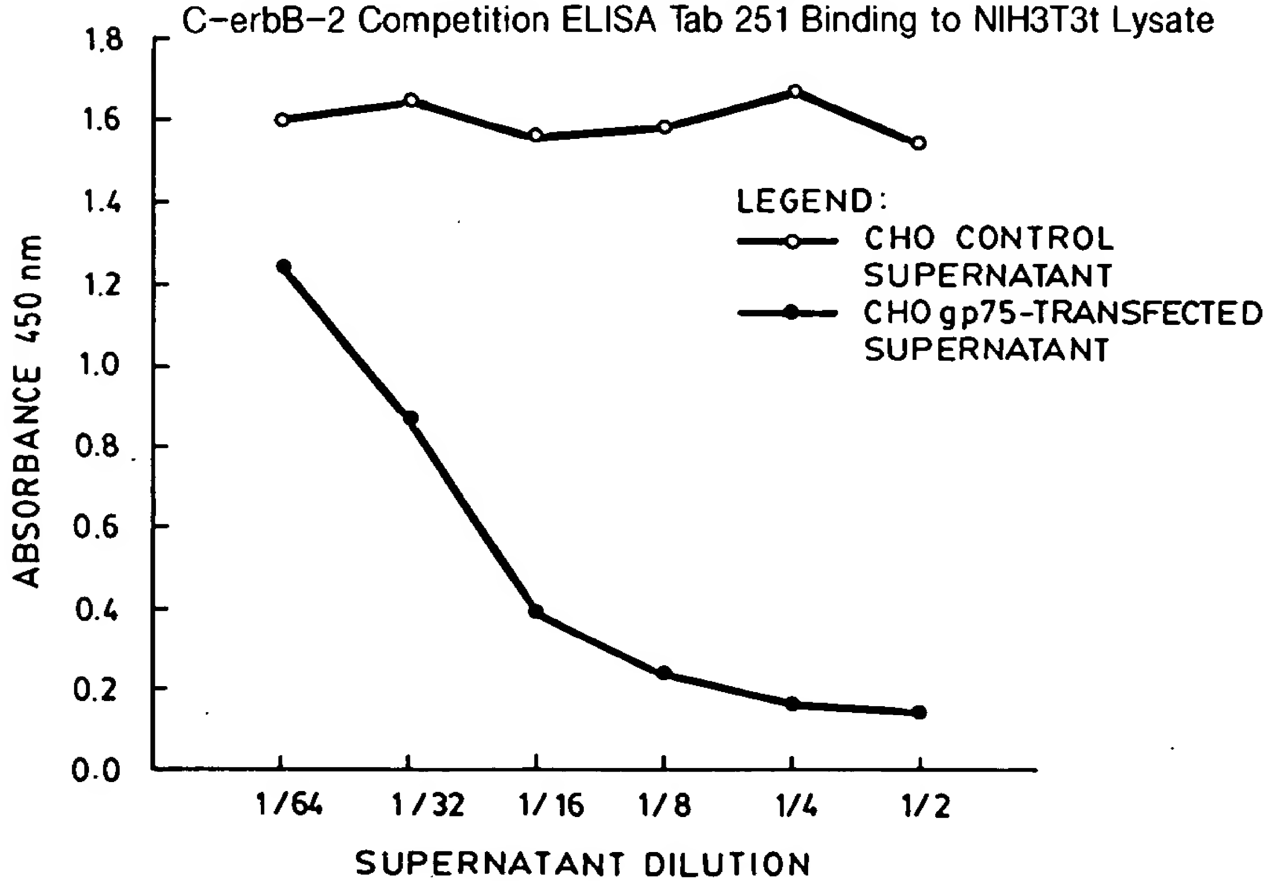
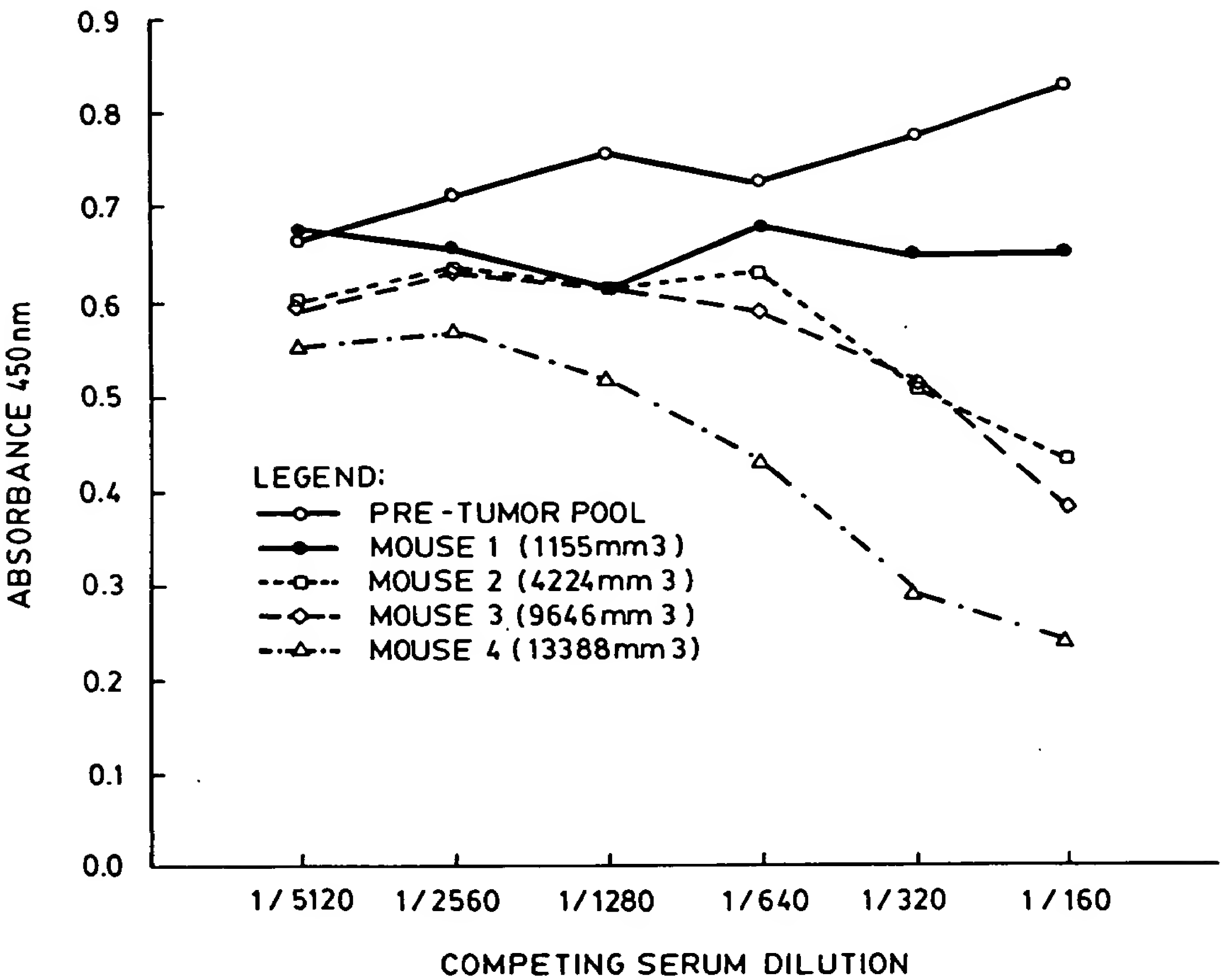


FIG. 15

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate



1 AATTCTCGAGCTCGTCGACCGGTCGACGAGCTCGAGGGTCGACGAGC

1 10
MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLe
151 ATGGAGCTGGCGGCCTTSTGCCGCTGGGGGCTCCTCCTCGCCCTCTT

60
GlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThrTyrLeuPr
301 CAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAACTCACCTACCTGCC

110
IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaVa
451 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGT

160
GlyGlyValLeuIleGlnArgAsnProGlnLeuCysTyrGlnAspTh
601 GGAGGGGTCTTGATCCAGCGGAACCCCCAGCTCTGCTACCAGGACAC

210
GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuTh
751 GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTCAGAGCCTGAC

260
AspCysLeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLe
901 GACTGCCTGGCCTGCCTCCACTTCAACCACAGTGGCATCTGTGAGCT

310
TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysPr
1051 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCC

360
ArgGluValARgAlaValThrSerAlaAsnIleGlnGluPheAlaGl
1201 CGAGAGGTGAGGGCAGTTACCAGTGCCAATATCCAGGAGTTTGCTGG

410
GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpPr
1351 GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCC

460
SerTrpLeuGlyLeuArgSerLeuArgGluLeuGlySerGlyLeuAl
1501 AGCTGGCTGGGGCTGCGCTCACTGAGGGAACTGGGCAGTGGACTGGC

510
GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAl
1651 GAGGACGAGTGTGTGGGCGAGGGCCTGGCCTGCCACCAGCTGTGCGC

560
ProArgGluTyrValAsnAlaArgHisCysLeuProCysHisProGl
1801 CCCAGGGAGTATGTGAATGCCAGGCACTGTTTGCCGTGCCACCCTGA

610
ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPh
1951 CCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTT

FIG. 16A

TCGAGGGCGCGCGCCCGGCCCCCACCCCTCGCAGCACCCCGCGCCCCCGC

20 30
uProProGlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLe
GCCCCCCGGAGCCGCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCT

70 80
oThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTy
CACCAATGCCAGCCTGTCCTTCCTGCAGGATATCCAGGAGGTGCAGGGCTA

120 130
lLeuAspAsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSe
GCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTC

170 180
rIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeuThrLe
GATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCTCTCACACT

220 230
rArgThrValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProTh
GCGCACTGTCTGTGCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCAC

270 280
uHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMetPr
GCACTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGAGTCCATGCC

320 330
oLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgCysGluLy
CCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAA

370 380
yCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPheAspGl
CTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGCTTTGATGG

420 430
oAspSerLeuProAspLeuSerValPheGlnAsnLeuGlnValIleArgGl
GGACAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGG

470 480
aLeuIleHisHisAsnThrHisLeuCysPheValHisThrValProTrpAs
CCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTGCCCTGGGA

520 530
aArgArgAlaLeuLeuGlySerGlyProThrGlnCysValAsnCysSerGl
CCGCAGGGCACTGCTGGGGTCAGGGCCCACCCAGTGTGTCAACTGCAGCCA

570 580
uCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAlaAspGl
GTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAGGCTGACCA

620 630
eProAspGluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSe
TCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTGCACCCACTC

FIG. 16B

CCTCCCAGCCGGGTCCAGCCGGAGCCATGGGGCCGGAGCCGCAGTGAGCACC

40 50

uArgLeuProAlaSerProGluThrHisLeuAspMetLeuArgHisLeuTyr

GCGGCTCCCTGCCAGTCCCGAGACCCACCTGGACATGCTCCGCCACCTCTAC

90 100

rValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg

CGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGG

140 150

rProGlyGlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLys

CCCAGGAGGCCTGCGGGAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAA

190 200

uIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys

GATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG

240 250

rAspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSer

TGACTGCTGCCATGAGCAGTGTGCTGCCGGCTGCACGGGCCCCAAGCACTCT

290 300

oAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro

CAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCC

340 350

sCysSerLysProCysAlaArgValCysTyrGlyLeuGlyMetGluHisLeu

GTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTG

390 400

yAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe

GGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT

440 450

yArgIleLeuHisAsnGlyAlaTyrSerLeuThrLeuGlnGlyLeuGlyIle

ACGAATTCTGCACAATGGCGCCTACTCGCTGACCCTGCAAGGGCTGGGCATC

490 500

pGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro

CCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA

540 550

nPheLeuArgGlyGlnGluCysValGluGluCysArgValLeuGlnGlyLeu

GTTCCTTCGGGGCCAGGAGTGCGTGGAGGAATGCCGAGTACTGCAGGGGCTC

590 600

nCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys

GTGTGTGGCCTGTGCCCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGC

640 650

rCysValAspLeuAspAspLysGlyCysProAlaGluGlnArgAlaSerPro

CTGTGTGGACCTGGATGACAAGGGCTGCCCCGCCGAGCAGAGAGCCAGCCCT

FIG. 16C

660
LeuThrSerIleValSerAlaValValGlyIleLeuLeuValValVa
2101 CTGACGTCCATCGTCTCTGCGGTGGTTGGCATTCTGCTGGTCGTGGT

710
ThrProSerGlyAlaMetProAsnGlnAlaGlnMetArgIleLeuLy
2251 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAA

760
AlaIleLysValLeuArgGluAsnThrSerProLysAlaAsnLysGl
2401 GCCATCAAAGTGTTGAGGGAAAACACATCCCCCAAAGCCAACAAAGA

810
MetProTyrGly$\boxed{\text{Cys}}$LeuLeuAspHisValArgGluAsnArgGlyAr
2551 ATGCCCTATGGC$\boxed{\text{TGC}}$CTCTTAGACCATGTCCGGGAAAACCGCGGACG

860
ValLeuValLysSerProAsnHisValLysIleThrAspPheGlyLe
2701 GTGCTGGTCAAGAGTCCCAACCATGTCAAAATTACAGACTTCGGGCT

910
HisGlnSerAspValTrpSerTyrGlyValThrValTrpGluLeuMe
2851 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGAT

△

ValTyrMetIleMetValLys$\boxed{\text{Cys}}$TrpMetIleAspSerGlu$\boxed{\text{Cys}}$Ar
3001 GTCTACATGATCATGGTCAAA$\boxed{\text{TGT}}$TGGATGATTGACTCTGAA$\boxed{\text{TGT}}$CG

1010
AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAs
3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGA

1060
SerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSe
3301 TCTACCAGGAGTGGCGGTGGGGACCTGACACTAGGGCTGGAGCCCTC

1110
LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspPr
3451 CTCCCCACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCC

1160
SerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaTh
3601 TCGCCCCGAGAGGGCCCTCTGCCTGCTGCCCGACCTGCTGGTGCCAC

1210
GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAl
3751 GGAGGAGCTGCCCCTCAGCCCCACCCTCCTCCTGCCTTCAGCCCAGC

1255
LeuAspValProValEND
3901 CTGGACGTGCCAGTGTGAACCAGAAGGCCAAGTCCGCAGAAGCCCTG
4051 CTAAGGAACCTTCCTTCCTGCTTGAGTTCCCAGATGGCTGGAAGGGG
4201 CCCTTTCCTTCCAGATCCTGGGTACTGAAAGCCTTAGGGAAGCTGGC
4351 ATGGTGTCAGTATCCAGGCTTTGTACAGAGTGCTTTTCTGTTTAGTT
4501 TTGTCCATTTGCAAATATATTTTGGAAAACAAAAAAAAAAAAAA

FIG. 16D

670 680
lLeuGlyValValPheGlyIleLeuIleLysArgArgGlnGlnLysIleAr
CTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATCCG

720 730
sGluThrGluLeuArgLysValLysValLeuGlySerGlyAlaPheGlyTh
AGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCAC

770 780
uIleLeuAspGluAlaTyrValMetAlaGlyValGlySerProTyrValSe
AATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCATATGTCTC

830
gLeuGlySerGlnAspLeuLeuAsnTrpCysMetGlnIleAlaLysGlyMe
CCTGGGCTCCCAGGACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGAT

870 880
uAlaArgLeuLeuAspIleAspGluThrGluTyrHisAlaAspGlyGlyLy
GGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGGCAA

920 930
tThrPheGlyAlaLysProTyrAspGlyIleProAlaArgGluIleProAs
GACTTTTGGGGCCAAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGA

970 980
gProArgPheArgGluLeuValSerGluPheSerArgMetAlaArgAspPr
GCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCCAGGGACCC

1020 1030
pLeuValAspAlaGluGluTyrLeuValProGlnGlnGlyPhePheCysPr
CCTGGTGGATGCTGAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCC

1070 1080
rGluGluGluAlaProArgSerProLeuAlaProSerGluGlyAlaGlySe
TGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGGGCTGGCTC

1120 1130
oThrValProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCy
CACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTTGCCCCCCTGACCTG

1170 1180
rLeuGluArgAlaLysThrLeuSerProGlyLysAsnGlyValValLysAs
TCTGGAAAGGGCCAAGACTCTCTCCCCAGGGAAGAATGGGGTCGTCAAAGA

1220 1230
aPheAspAsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaPr
CTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGAGCGGGGGGCTCC

ATGTGTCCTCAGGGAGCAGGGAAGGCCTGACTTCTGCTGGCATCAAGAGGT
TCCAGCCTCGTTGGAAGAGGAACAGCACTGGGGAGTCTTTGTGGATTCTGA
CTGAGAGGGGAAGCGGCCCTAAGGGAGTGTCTAAGAACAAAAGCGACCCAT
TTTACTTTTTTTGTTTTGTTTTTTAAAGACGAAATAAAGACCCAGGGGAG

FIG. 16E